

RESULT 1  
 US-09-818-780-89  
 ; Sequence 89, Application US/09818780  
 ; Patent No. 6677146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McHenry, Charles  
 ; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME  
 ; FILE REFERENCE: 1794.0030004  
 ; CURRENT APPLICATION NUMBER: US/09/818,780  
 ; CURRENT FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/192,736  
 ; PRIOR FILING DATE: 2000-03-28  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 89  
 ; LENGTH: 305  
 ; TYPE: PRT  
 ; ORGANISM: Aquifex aeolicus  
 US-09-818-780-89

Query Match 100.0%; Score 1570; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-142;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      301 AVQAD 305
  
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RESULT 1  
 D70432  
 conserved hypothetical protein aq\_1526 - Aquifex aeolicus  
 C;Species: Aquifex aeolicus  
 C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C;Accession: D70432

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.  
 Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 A;Accession: D70432  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-305  
 A;Cross-references: UNIPROT:O67486; UNIPARC:UPI000004350C; GB:AE000744; NID:g2983891; PIDN:AAC07454.1; PID:g2983903; GB:AE000657  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: aq\_1526

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Query Match          100.0%;   Score 1570;   DB 2;   Length 305;
Best Local Similarity 100.0%;   Pred. No. 1.8e-92;
Matches 305;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1 MEKVFLQKTLHIPGGLLFYKGEGSGTKTAFEFAGILCKENVPGCGSCPCKHVN 60
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Qy      61 ELEEAFKGEIEDFKVYKDKGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
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Qy      121 KPALSRRKVIIDDAHAMTSQAANALLKVLEPPADTTILTNRRAILPTILSRFTQV 180
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Db      121 KPALSRRKVIIDDAHAMTSQAANALLKVLEPPADTTILTNRRAILPTILSRFTQV 180

Qy      181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS 240
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Db      181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS 240

Qy      241 EFEKWEPEKQKLFLEIMEELVSQKLTEKKDNYTYLLDTIRLFKDLARGVNEPLWLFTL 300
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Db      241 EFEKWEPEKQKLFLEIMEELVSQKLTEKKDNYTYLLDTIRLFKDLARGVNEPLWLFTL 300

Qy      301 AVQAD 305
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Db      301 AVQAD 305
  
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RESULT 1
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ID   O67486_AQUAE PRELIMINARY;          PRT;   305 AA.
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DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein aq_1526.
GN   OrderedLocusNames=AQ_1526;
OS   Aquifex aeolicus.
OC   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
  
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OX NCBI\_TaxID=63363;  
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 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 DR EMBL; AE000744; AAC07454.1; -; Genomic\_DNA.  
 DR PIR; D70432; D70432.  
 DR HSSP; P06710; 1NJF.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR SMART; SM00382; AAA; 1.  
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.  
 SQ SEQUENCE 305 AA; 34897 MW; 2B207935455B7E8A CRC64;

Query Match 100.0%; Score 1570; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-91;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEKVFLKQLKTLHIPGGLLFYKGEGSGTKTAFEFAGILCKENVPWGCSCPCSKHVN 60
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Db      1 MEKVFLKQLKTLHIPGGLLFYKGEGSGTKTAFEFAGILCKENVPWGCSCPCSKHVN 60

Qy     61 ELEEAFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
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Qy    121 KPALSRRKVIIIDAHAMTSQAANALLKVLEPPADTTFTILTNRRAISAILPTILSRFQV 180
      |||
Db    121 KPALSRRKVIIIDAHAMTSQAANALLKVLEPPADTTFTILTNRRAISAILPTILSRFQV 180

Qy    181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLAS 240
      |||
Db    181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLAS 240

Qy    241 EFEKWEPEKQKLFLEIMEELVSQKLTEKKDNYTYLLDTIRLFKDGDLARGVNEPLWLFTL 300
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Qy    301 AVQAD 305
      ||||
Db    301 AVQAD 305
  
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STN SEARCH:

(FILE 'HOME' ENTERED AT 14:57:48 ON 01 DEC 2008)

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOTECHNO, EMBASE, JAPIO' ENTERED AT  
15:00:53 ON 01 DEC 2008

L1            217 S AQUIFEX AND POLYMERASE  
L2            110 DUP REM L1 (107 DUPLICATES REMOVED)  
L3            9 S L2 AND DELTA